46

RAW SEQUENCE LISTING PATENT APPLICATION US/08/656,811A

DATE: 02/07/97 TIME: 16:32:23

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This Raw Listing contains the General Information Section and up to the first 5 pages.

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ENTERED SEQUENCE LISTING 1 2 3 General Information: (1) 5 (i) APPLICANT: Bartsch, Dusan Kandel, Eric R. 7 Ghirardi, Mirella 8 9 (ii) TITLE OF INVENTION: A METHOD FOR ENHANCING LONG-TERM MEMORY IN A 10 SUBJECT AND USES THEREOF 11 12 (iii) NUMBER OF SEQUENCES: 20 13 (iv) CORRESPONDENCE ADDRESS: 14 15 (A) ADDRESSEE: Cooper & Dunham LLP (B) STREET: 1185 Avenue of the Americas 16 17 (C) CITY: New York 18 (D) STATE: New York 19 (E) COUNTRY: U.S.A. 20 (F) ZIP: 10036 21 (v) COMPUTER READABLE FORM: 22 23 (A) MEDIUM TYPE: Floppy disk 24 (B) COMPUTER: IBM PC compatible 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 27 28 (vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: 29 30 (B) FILING DATE: 31 (C) CLASSIFICATION: 32 33 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: White, John P. 34 35 (B) REGISTRATION NUMBER: 28,678 36 (C) REFERENCE/DOCKET NUMBER: 50865/JPW/JML 37 38 (ix) TELECOMMUNICATION INFORMATION: 39 (A) TELEPHONE: 212-278-0400 40 (B) TELEFAX: 212-391-0525 41 42 43 (2) INFORMATION FOR SEQ ID NO:1: 44 45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

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47		(B)	TYI	PE: 8	amino	ac:	id									
48		(C) STRANDEDNESS: single														
49		(D)	TOI	POLO	GY: 3	linea	ar			•	•					
50																
51	(ii)	MOLE	ECULI	TYI	PE: 1	pept:	ide									
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53																
54																
55																
56	(xi)	SEOU	JENCI	E DES	SCRI	PTIO	N: SI	EO II	ONO:	:1:						
57	(/	_						_								
58	Met	Glu	Leu	Asp	Leu	Trp	Ser	Glu	Asp	Phe	Gln	Leu	Ala	Arq	Glu	Trp
59	1			<i>E</i>	5					10					15	-
60	_				_					- •						
61	Glv	T.eu	Glu	Met	Pro	Val	Val	Gln	Thr	Asp	Glv	Gln	Phe	Ġlv	Asp	Leu
62	017			20					25	F	1			30	E	
63				20												
64	Luc	Sar	Thr	Ser	Arg	Hie	Glv	Glv	Asn	Glu	Ser	T.eu	Ser	T.e.11	Gln	Pro
65	цуз	261	35	261	Arg	1113	GLY	40	ASP	01.0	Der	пса	45	пса	O ±11	110
66			33					40					43			
67	al n	a1	A 7 a	mb ~	Leu	Tuc	LON	Clu	Dro	Pho	Glu	Glu	λen	Val	T 011	Gl v
68	GIII	-	АТа	1111	теп	ьуъ	55	GIU	FIO	FILE	GIU	60	АЗР	Val	nea	GLY
		50					23					00				
69	31-	a1	m	16-4	a 1	C	C	3 ~~	T 011	a1	Co=	Dho	T 011	A an	7 T A	T 011
70		GIU	ттр	мес	Glu		ser	ASP	rea	СТУ			ьeu	ASP	Ата	80
71	65					70					75 .					80
72	a1	•	•	***	a1	•	.	***	D	Dh.	~1	G	3	T	T	a1
73	GTÀ	Asp	Asn	HIS	Glu	Arg	ren	HIS	Pro		GTU	Ser	Asn	Leu		GIU
74					85					90					95	
75				_		_,	_	_	_		-1		_	_	•	-1-
76	Phe	Thr	Ser		Ile	Thr	Pro	Asp		ser	Thr	vaı	ser	_	Asp	тте
77				100					105					110		
78	_			_,	_			_	1	~ 7	_			-7-	.	.
79	Leu	Ser		Thr	Leu	GIn	Pne		Thr	GIN	Pro	vaı		тте	Pro	Leu
80			115					120					125			
81							9	_	_,	_			_,			~ 7
82	Tyr		Ser	His	Gly	Ala		Asp	Phe	Ser	Ala		Thr	GIU	Phe	GIU
83		130					135					140				
84		_												_	-	
85		His	Leu	Ser	Pro		Asp	Ser	Pro	Glu		Val	Ala	Pro	Val	
86	145					150					155					160
87																
88	Asn	Leu	Glu	Pro	Val	Glu	Leu	Thr	Ala	Ser	His	Met	Thr	Val	Ile	Ser
89					165					170					175	
90																
91	Pro	Asp	Gly	Leu	Leu	Gly	Gly	Met	Glu	Leu	Ala	Ser	Glu	Ser	Leu	Thr
92				180					185					190		
93																
94	Phe	Thr	Glu	Leu	Asp	Phe	Val	Asn	Phe	Asn	Asp	Ser	Ala	Val	Gly	Ser
95			195		_			200			_		205			
96																
97	Ile	Gly	Gly	Ala	Glu	Glu	Leu	Leu	Gly	Ser	Pro	Leu	Ser	Val	Asp	Asp
98		210	-				215		_			220			_	_
99																

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100	Vá	al	Glu	Ser	Thr	Ile	Ser	Phe	Ser	Gly	Pro	Ser	Ser	Pro	Glu	Thr	Ser
101	22	25					230			_		235					240
102																	
103	G]	ln	Ser	Ser	Ile	Ile	Glu	Ser	Ser	Pro	Glu	Leu	Tyr	Lys	Val	Ile	Ser
104						245					250		_	_		255	
105																	
106	Tł	nr	Ser	Ser	Ilė	Asp	Ala	Ser	Lys	Arg	Phe	Ser	Pro	Tyr	Ser	Arg	Ser
107					260	_				265					270		
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109	Se	er	Lys	Ser	Lys	Gln	Ser	Val	Lys	Thr	Ser	Asp	Ala	Lys	Ala	Pro	Arg
110				275					280					285			
111																	
112	L			Arg	Thr	Pro	Ala	Gln	Pro	Val	Pro	Glu	His	Val	Ile	Met	Glu
113			290					295					300				
114																	
115			Leu	Asp	Lys	Lys	Asp	Arg	Lys	Lys	Leu		Asn	Lys	Asn	Ala	Ala
116	30)5					310					315					320
117	_									_	_	_	_	_	_		
118	I]	Le	Arg	Tyr	Arg		Lys	Lys	Lys	Gly		Ala	Gln	Gly	Ile	_	Gly
119						325					330					335	
120						_			_	_		_	_	_		_	
121	G.	Lu	GLu	GIn		Leu	GLu	Glu	Leu		Thr	Lys	Leu	Lys		Lys	Val
122					340					345					350		
123	_			_	43				_	_		-		_		~7	_
124	AS	sp	Asp		GIN	Arg	GIU	Ile	_	Tyr	мет	гàг	Asn		мет	GIU	Asp
125				355		•			360					365			
126	***	. 1	a	T	.1.	T	a 1	-1 -	a 1	T	T	.					-
127 128	Vā			ràs	АТа	гàг	GTÀ	Ile	GIN	Leu	ràs	мет					
128			370					375									
130																	
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144	(xi	L)	SEQU	JENCE	DES	CRIE	PTION	V: SI	EQ II	ON C	:2:						
145																	
146	Le	eu .	Asp	Lys	Lys	Asp	Arg	Lys	Lys	Leu	Gln	Asn	Lys	Asn	Ala	Ala	Ile
147	1					5					10					15	
148																	
149	Ar	g	Tyr	Arg	Met	Lys	Lys	Lys	Gly	Glu	Ala	Gln	Gly	Ile	Lys	Gly	Glu
150					20					25					30		
151																	
152	Gl	Lu	Gln	Glu	Leu	Glu	Glu	Leu	Asn	Thr	Lys	Leu	Lys	Thr	Lys	Val	Asp

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Asp Leu Gln Arg Glu Ile Lys Tyr Met Lys Asn Leu Met Glu Asp Val Cys Lys Ala Lys Gly Ile Gln Leu Lys (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: TGACGTCA (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AGTATTGCGT CATC (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

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209
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
210
211
     ACTATTGCGC AATC
                                                                                 14
212
      (2) INFORMATION FOR SEQ ID NO:6:
213
214
215
           (i) SEQUENCE CHARACTERISTICS:
216
                (A) LENGTH: 20 base pairs
217
                (B) TYPE: nucleic acid
218
                (C) STRANDEDNESS: single
219
                (D) TOPOLOGY: linear
220
221
          (ii) MOLECULE TYPE: DNA (genomic)
222
223
224
225
226
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
227
     TTCCGCTTTC CATAAGTCGA
228
                                                                                 20
229
      (2) INFORMATION FOR SEQ ID NO:7:
230
231
232
           (i) SEQUENCE CHARACTERISTICS:
233
                (A) LENGTH: 20 base pairs
234
                (B) TYPE: nucleic acid
235
                (C) STRANDEDNESS: single
236
                (D) TOPOLOGY: linear
237
238
          (ii) MOLECULE TYPE: DNA (genomic)
239
240
241
242
243
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
244
245
     ACCTGAAAAT GATATTGTAC
                                                                                 20
246
      (2) INFORMATION FOR SEQ ID NO:8:
247
248
249
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 37 base pairs
250
251
                (B) TYPE: nucleic acid
252
                (C) STRANDEDNESS: single
253
                (D) TOPOLOGY: linear
254
255
          (ii) MOLECULE TYPE: DNA (genomic)
256
257
258
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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/656,811A

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